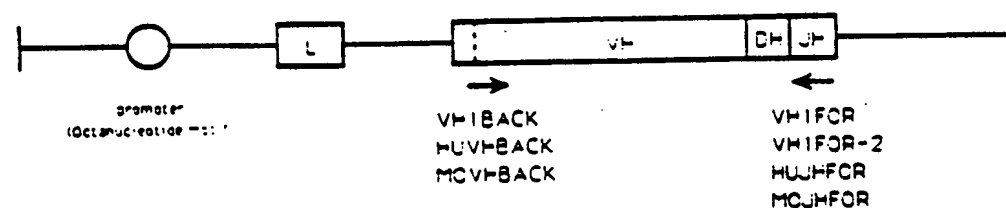
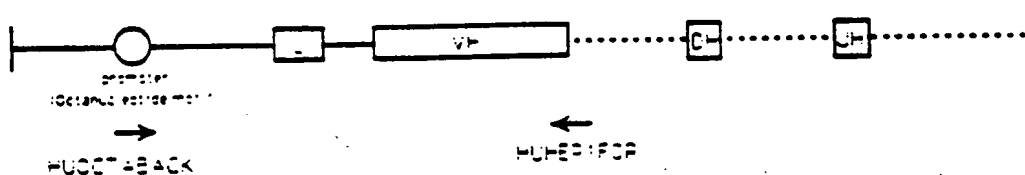


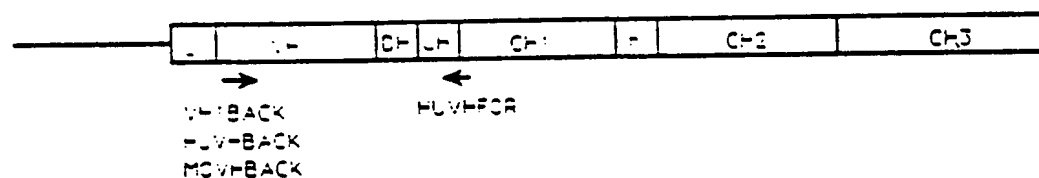
Rearranged heavy chain variable gene (DNA)



Unrearranged heavy chain variable gene (DNA)



Rearranged heavy chain variable gene (mRNA)



Rearranged light chain variable gene (DNA)

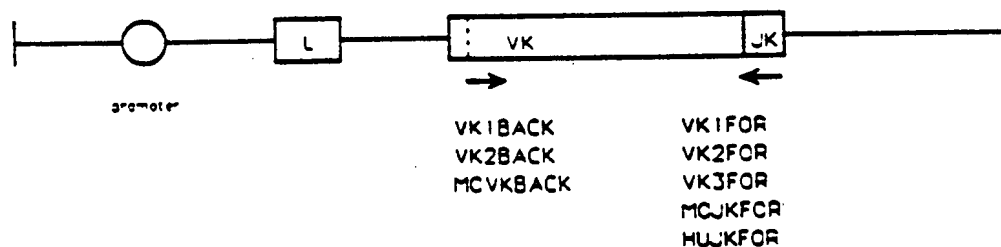


FIG. 1

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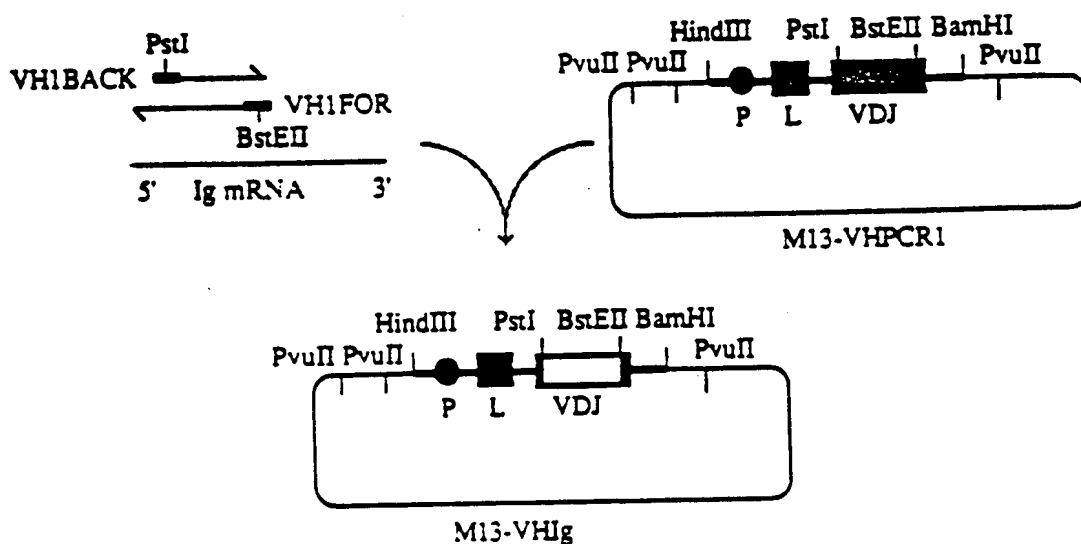


FIG. 2

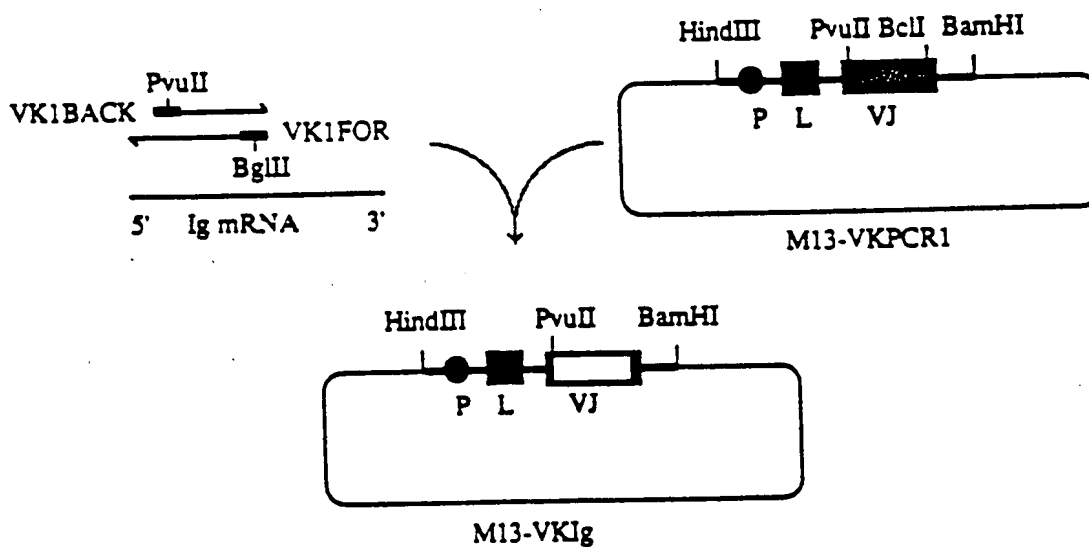


FIG. 4

00377-4962260

HLA-DI 11

AAGATGAATATGCAATCTCTGAACTACATGGTAAATATAGGTTGTCTATCCA
10 20 30 40 50 60

CAAACGAAACATGATACAGTTTCTACAGTACTGAGACACAGGACCTAC
 70 80 90 100 110 120

M G W S C I I L F L V A T A T
CATGGGATGGAGCTTCTATACCTCTTTTGGTAGCAACAGCTACAGGTAGGGGGCTCAC
130 140 150 160 170 180

AGTAGAGGCTGAGCTTGACATATATGGGTGACATGACATTCACCTTTCCTTC
190 200 210 220 230 240

PstI
 51
 10
 G V H S Q V Q L Q E S G P G L V R P
 TTTTACAGGCTTTCACCTGAGTTCACAGGAGCGGTCAGGCTGTGTGAGAC
 250 255 270 280 290 300

CDR1

15 20 25 30
S Q T L S L T C T V S G S T F S S Y W M
CTAGCCAGACCCCTGAGCTGACCTGCAAGCTCTGTGGCAGCACCCTCAGCAGCTACTGGA
310 320 330 340 350 360

CDR2

35 40 45 50

H W V R Q P P G R G L E W I G R I D P N

TGCAC TGGGTGAGACAGCCACCTGGACAGAGTCTTGAGTGGATTGGAAGGATGATGCTTA

370 380 390 400 410 420

55 60 65 70
S G G T K Y N E K F K S R V T M L V D T
A T A G T G T G T A C T A A G T A C A A T G A G A G T T A A G A G C A G A G T G A C A A T G C T G G T A G A C A
430 440 450 460 470 480

75 80 85 90
 S K N Q F S L R L S S V T A A D T A V Y
 CGACGACGACCGAGCTTCAGCTGAGACTGACAGCGGTGACAGCGCGGACACCGGGGTCT
 490 500 510 520 530 540

CDR3

95 100 105 110

Y C A R Y D Y Y G S S Y F D Y W G Q G T

ATTATTGTGCAAGATACGATCTACTACGGTAGCTACTTTGACTACTGGGGCCAAGGGA

550 560 570 580 590 600

BstEII
 115 | 120
 T V T V S S
 CCACGCTTACCGTCTCTCTCAGGTGAGTCTTACAACGCTCTCTCTTCTATTGAGCTTAAAT
 610 620 630 640 650 660

AGA...TACTGCA...TTGTGGGGGGAAATGTGTGATCTGAA...TTCAGGTCAAGAAGGA
670 680 690 700 710 720

CTAGGGACACCTTGGGAGTCAGAAAGGTCATTGGGAGCCCGGGCTGATGCAGACAGACA
730 740 750 760 770 780

BamHI

TCTCAGCTCCCAAGACTTCAATGCCAGAGATTATAG
 790 800 810

FIG. 3

06244-1600

ML3_VkPCR1

Hand III

38 48 58 68 78 88

CAAACAGAAAACATGAGATACAGTCTTTTACAGTTACTGAGCACAGGACCTCAC
98 108 118 129 138 148

M G W S C I I I F I V A T A T
 CATGGGATGGAGCTGATACAGGGCTTTTGTATGACAGCTACAGTAAAGGGGCTCAC
 158 168 178 188 198 208

AGTAGCAGGCTTGAGGTCGGACATATAAGGTTACCAATGACATCCACTTTCGCTTTC
218 228 238 248 258 268

25 88

G V H S D : Q L : G S P S S L S A S

15 25 35 45 55 65 75 85 95 105 115 125 135 145 155 165 175 185 195 205 215 225 235 245 255 265 275 285 295 305 315 325 335 345 355 365 375 385 395 405 415 425 435 445 455 465 475 485 495 505 515 525 535 545 555 565 575 585 595 605 615 625 635 645 655 665 675 685 695 705 715 725 735 745 755 765 775 785 795 805 815 825 835 845 855 865 875 885 895 905 915 925 935 945 955 965 975 985 995
 V G D R V I T C R A S G N I H N Y L A
 GCTGGGTGCACAGCTGACGATCCTGCTTATGACGAGCGGTACATTCACAACTACCTGG
 338 345 352 368 378 388

CDR2

35 40 45 50

W Y Q Q K P G K A F K L L I Y Y T T T L

CTTGGTACCAAGCAGAGAGCGGTAGCGCTCAAGCTGCTGATCTACTACACCACCAACCC

198 408 418 428 438 448

5' 60 65 70
 A C G V P S R F S G S G S G T D F T F T
 TGGCTACGGGTGCGCAGCAGATTACGGGTACGGGTACGGGTACCGACTTCACCTTCA
 458 468 478 488 498 508

CDR3

75 80 85 90

T S S L Q P E D I A T Y Y C Q H F W S T

CCATCAGCAGCGCTCCAGCCAGAGGACATCGCCACCTACTACTGCCAGCACTTCTGGAGCA

518 528 538 548 558 568

Bcl I (requires dam⁻ host)

95 100 105 108
 P R T F G Q G T K V V I K R
 CCCAAGGACGTTCCGCGCAGGGACCAAGTGGGATCGACCGTGTAGAACTTAAAC
 578 589 598 608 618 628

පිළිගැනීම

628 348

FIG. 5

11771 11772 11773 11774 11775 11776 11777 11778 11779 11780 11781 11782 11783 11784 11785 11786 11787 11788 11789 11790 11791 11792 11793 11794 11795 11796 11797 11798 11799 11800 11801 11802 11803 11804 11805 11806 11807 11808 11809 11810 11811 11812 11813 11814 11815 11816 11817 11818 11819 11820 11821 11822 11823 11824 11825 11826 11827 11828 11829 11830 11831 11832 11833 11834 11835 11836 11837 11838 11839 11840 11841 11842 11843 11844 11845 11846 11847 11848 11849 11850 11851 11852 11853 11854 11855 11856 11857 11858 11859 11860 11861 11862 11863 11864 11865 11866 11867 11868 11869 11870 11871 11872 11873 11874 11875 11876 11877 11878 11879 11880 11881 11882 11883 11884 11885 11886 11887 11888 11889 11890 11891 11892 11893 11894 11895 11896 11897 11898 11899 11900 11901 11902 11903 11904 11905 11906 11907 11908 11909 11910 11911 11912 11913 11914 11915 11916 11917 11918 11919 11920 11921 11922 11923 11924 11925 11926 11927 11928 11929 11930 11931 11932 11933 11934 11935 11936 11937 11938 11939 11940 11941 11942 11943 11944 11945 11946 11947 11948 11949 11950 11951 11952 11953 11954 11955 11956 11957 11958 11959 11960 11961 11962 11963 11964 11965 11966 11967 11968 11969 11970 11971 11972 11973 11974 11975 11976 11977 11978 11979 11980 11981 11982 11983 11984 11985 11986 11987 11988 11989 11990 11991 11992 11993 11994 11995 11996 11997 11998 11999 12000

Splice -1
↓ G V H S
AGGTGTCCACTCC

Sequence of MB-1 VK

Splice -1
↓ G V H S
AGGTGTCCACTCC

FIG. 6

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α -Lys 30

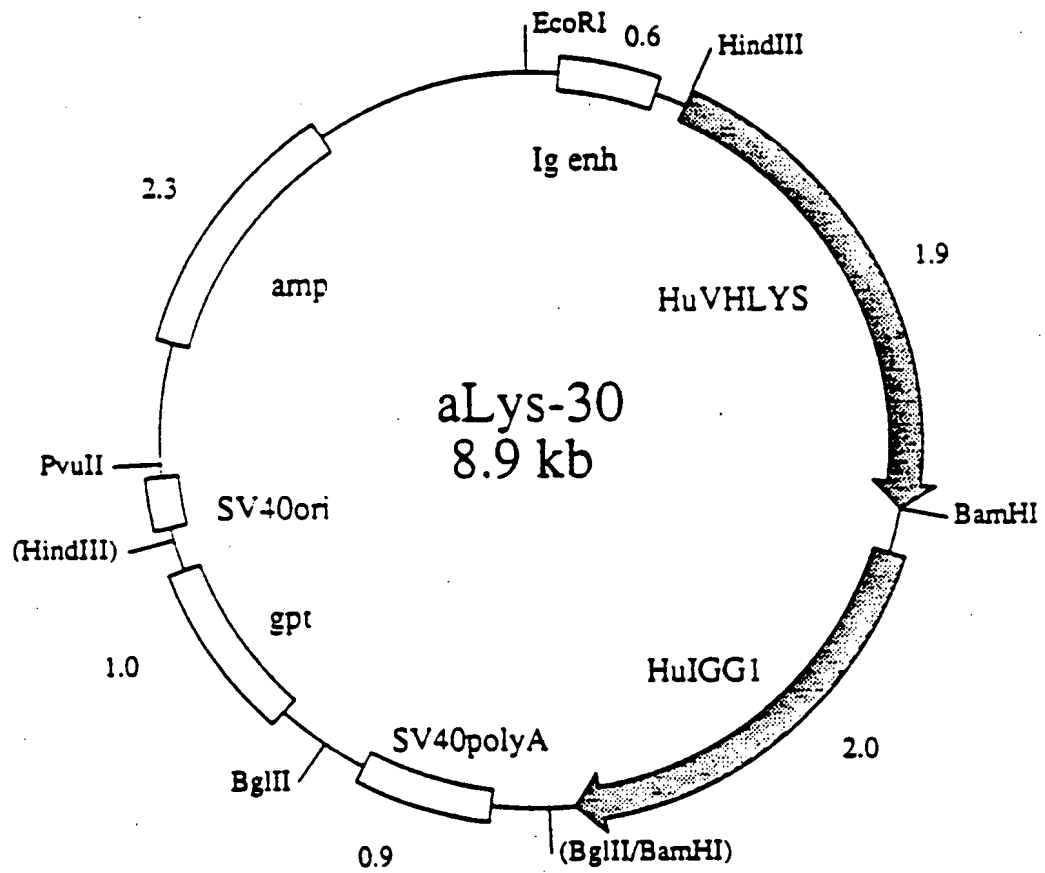


FIG. 7

α -Lys 17

7/23

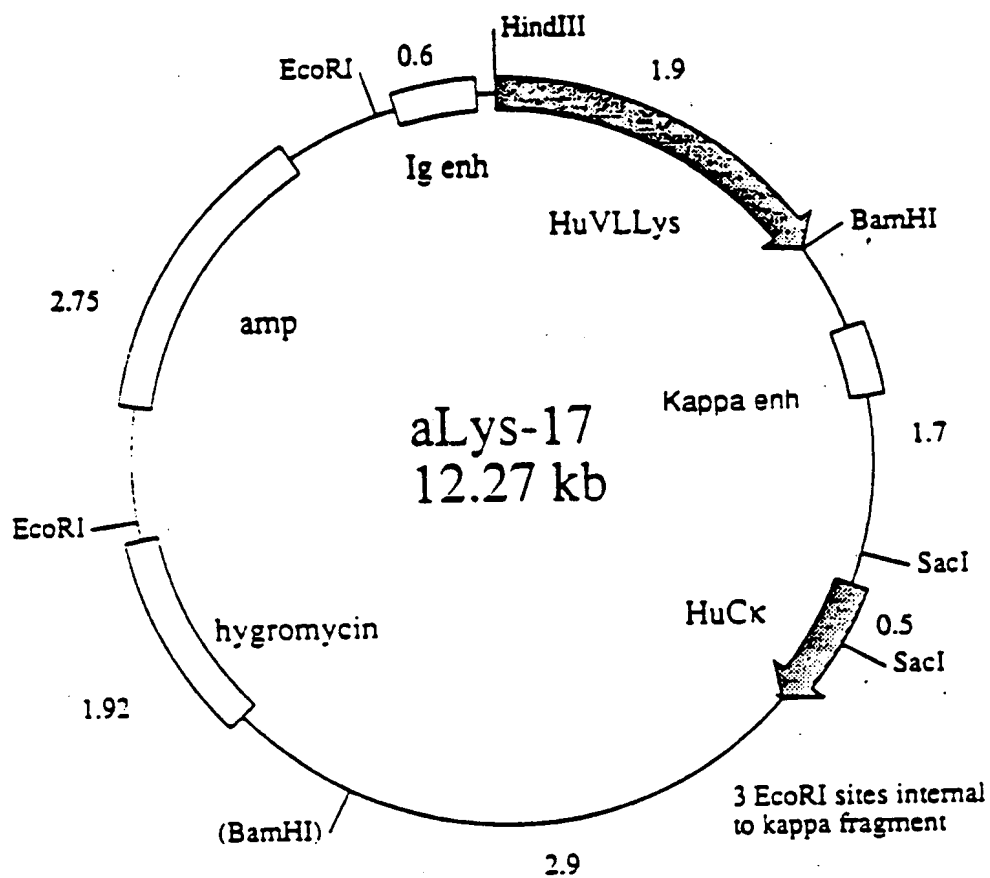


FIG. 8

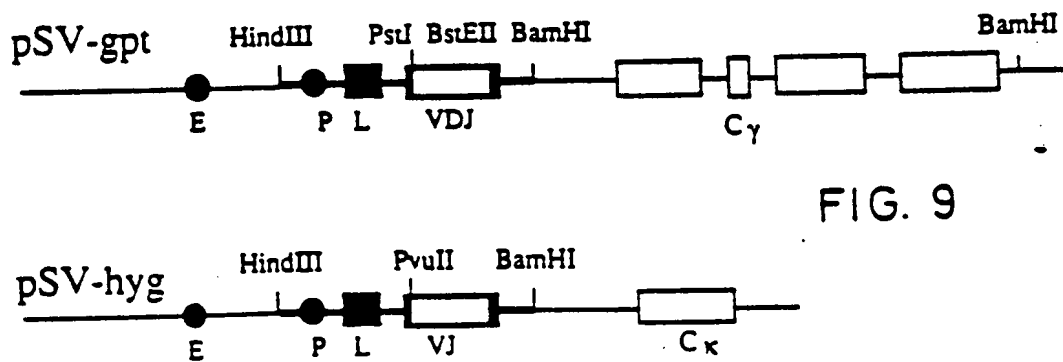


FIG. 9

ZENWZFAV
 ZRZLGFNTAV
 ZSSGSZVY
 VSSGYSZVY

HGDSSSXYFY
 NGGY
 LGROYAMY
 KROYOYRGYYYAMY
 YDGSFTAY
 EGYGYFAY
 YHYDSSSYYAMY
 13 00.
 21 00.
 29 00.
 37 00.
 32 00.

Ps.gene/Unproductive
Unproductive
Unproductive
Unproductive
Unproductive

100

Unproductive
Unproductive

RELAYAND
VYENEFAY
EINAKUYVENOV
XXYYXAYOY
SSOOYD
GAARATWAY
GGFAY
SPHAY
EIVGOGFYATOY
MXYGGSLATAY
KVVAYDY
KGWSTVFON
TGFAY
24 NO.
9 NO.
20 NO.
18 NO.

Ps.gene
Ps.gene/Unproductive
Unproductive
Unproductive
Unproductive

WILGAMY
GYYVDCSYVAMY
ZJ 02.

Unproductive

AKENLYFDY
RECVESRLOGOV
RGLHNFDP
RNYGSSPFDY
PPHMFSSY
43 02.
28 02.
35 02.

Ps.gene
Ps.gene
Ps.gene
Ps.gene
Ps.gene/'Unproductive'
Ps.gene/'Unproductive'
Unproductive

3C 22.

Unproductive

#REF33342:

FIG. 10b

10/23

CDR 2FRAMWORK 3CDR 3

KABAT HUMAN VH1

	STSTAYMELRSLRSED	AVYYCAR	GEGWQHFDY
HACKFQG	RVTIRRHKSTSTAYMELSSLRSED	AVYYCAR	GSRYGYDCSGYYL
GYACKFQG	RVTMRRTSTSTAYMELSSLRSED	AVYYCAR	LAHFSGSPVDWDF

KABAT HUMAN VH2

KHQLQPSLKS	RVTISVDTSKNQFSLKLSSTAA	DTAVYYCAR	GGVPPAAMDV
KS	RVTISVDTSKNQFSLKLSSTAA	DTAVYYCAR	MARYYDFWSGYSAYDY
SLKS	RLSISQDTSPNQFSLRLSSTAA	DTAVYYCAR	HRNWGSPVHFDY
	ESTSTAYMELSSLRSED	AVYYCAR	DSYGQYGGHY

KABAT HUMAN VH3

ISYITSSSSYNYADSVKG	RFTISRDNKNSLYLQMNSLRAED	TA	AVYYCAR	DGRFGTYSPSDY
SVKG	RFTISRDDSKSIAYLOVNSLKTED	TA	AVYYCTR	TIYYDSSGYPYW
YADSVKG	RFTISRDNKNSLYLQMNSLRAED	TA	FYYCAR	GIALDAFDI
YYADSVKG	RFTISRDNKNSLYLQMNSLRAED	TA	FYYCAK	53 NT. UNPROD REARR
DSVKG	RFTISRDNKNSLYLQMNSLRAED	TA	FYYCAR	DHSGTGGGGSGSYF
VSAISGSGGSTYYADSVKG	RFTISRDNPKNTLYLQMNSLRAED	TA	FYYCAR	KDNLWFD
AVISYDGSNKYYADSVKG	RFTISRDNKNTLYLQMNSLRAED	TA	FYYCAR	DLGGRGVVVVPAPGGRSIIYYGMDV
GAVISYDGSNKYYADSVKG	RFTISRDNKNTLYLQMNSLRAED	TA	FYYCAS	LEGIGTIYYYGMDV
	AKNSLYLQMNSLRAED	TA	FYYCVR	DDSSSWPKHFQ
QYAASTVKG	RFTISRDDSKNSLYLQMNSLNTED	TA	FYYCVR	SGVVPYLDY

KNOWN FAMILY

AVYYCAR	DPRIARPDYYYYMDV
TAVYYCAR	GAEVVEFTARYYYGLNV

FIG. 11

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FR1	CDR1	FR2
YTTT	SYGDS	WVTTSPWTRCLRWMG
GEKPGSSVKV/SCKASGYTFT	DYFMN	WMRCAPGGRLEWMG
QVQLQETIGPRTEASETTLSTLCAVSGDSIS	SGNW*1	WVRQPPGKGLEWIG
QVQLQESGPGLVK*SETTSLTCTVSGGSIS	SYIWS	WIRQPPGKGLEWIG
GYTFT	NYCMH	WVRQDHAQGLEWMG
QVQLQESGPGLVK*SETTSLYCAVSGDSIS	SGNW*1	WVRQPPGKGLEWIG
GPRLGEASETTLSTLCTVSGGSIS	SSSYW	WIRQPPGKGLEWIG
QVQLQESGPGLVK*SETTSLTCTVSGGSIS	SYIWS	WIRQPPGKGLEWIG
LSLCAVSGGSIS	SGNW*1	WVRQPPGKGLEWIG
SETTSLTCAVYGGSTF	GYIWS	WIRQPPGKGLEWIG
QVQLVQSGAEVKKPGASVKV/SCKASGYTFT	NYCMH	WVRQVLAQGLEWMG
SETTSLICAVSGDSIS	SGNW*1	WVRQPPGKGLEWIG
SRAQTGEASETTLSTLCTVSGGSIS	SSSYWG	WIRQPPGKGLEWIG
CPLTCTVSGGSVSSGS	YIWS	WIRQPPGKGLEWIG
GLVKPSETTSLTCTVSGGSIS	SYIWS	WIRQPPGKGLEWIG
SETTSLICAVSGDSIS	SGNW*1	WVRQPPGKGLEWIG
QVQLVQSGAEVKKPGSEVKV/SCKASGYTFT	SYALS	WVRQAPGQGLEWMG
QVQLQWAGLLKPSETTSLTCAVYGGSTF	GYIWS	WIRQPPGKGLEWIG
QVQLQESGPGLVKPSETTSLTCTVSGGSIS	SSSYWG	WIRQPPGKGLEWIG
GPGLVKPSETTSLTCTVSGGSIS	SSGYWS	WIRQPPGKGLEWIG

* indicates stop codon (unsure as sequence remains in frame)
 • sequence terminates due to internal restriction site
 lower case denotes frame shift

FR1	FR2	CDR3
WISAYNGNTNYAQKLG	RVTMTDTSTSTAYMELSLRSEDATVYYCAR	DTVSS
WISAGNGNTKYSCKLG	RVTITRDTSTASTAYMQLSSLRSEDATVYYCAR	DTVSS
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLS*	
RIYTSGSTNYNPSLKS	RVTISVDTSKNQFSLKLS SVTAADTAVYYCAR	DTVSS
LVCPSDGSTSYAQKFGA	RVTITRDTSMSTAYMELSSLRSEDATVYYCAR	DTVSS
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLS*	
EIHHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLS*	
YIYSGSTNYNPSLKS	RVTISVDTSKNQFSLKLS*	
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLS*	
EIHHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLS SVTAADTAVYYCAR	DTVSS
LVCPSDGSTSYAQKFGA	RVTITRDTSMSTAYMELSSLRSEDATVYYCAR	DTVSS
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLS*	
SIYSGSTYYNPSLKS	RVTIPVDTSKNQFSLKLS*	
YIYSGSTNYNPSLKS	RVTISVDTSKNQFSLKLS SVTAADTAVYYCAR	DTVSS
RIYTSGSTNYNPSLKS	RVTMSVDTSKNQFSLKLS*	
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLS*	
RIIPILGIANYAQKFGG	RVTITADKSTSTAYMELSSLRSEDATVYYCAR	DTVS
EIHHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLS*	
EIHHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLS*	
YIYSGSTYYNPSLKS	RVTISVDTSKNQFSLKLS SVTAADTAVYYCAR	DTVSS

FIG. 12

09722364-112800

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pSWL

HindIII site AAGCTT

M K Y L L P T A A
 GCATGCAAAATTTCTATTTTCAAGGAGACAGTCATAATGAAATACCTATTGGCTACGGCAGCC
 10 20 30 40 50 60

A S L L L L A A Q P A M A Q V Q L Q E S
 GCTGGATTGTTTATTACTGCGTGGCCCAACCAGCGATGGCCAGGTGCAGCTGCAGGAGTCA
 70 80 90 100 110 120

G F G L V A P S Q S L S I T C T V S G F
 GGACCTGGCGTGGTGGCGCGCTTCACAGAGCGTGTCCATCAGATGCACCGCTCTCAGGGTTC
 130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
 TCATTAACCGGTTATGGTGTAAATGGTTCGCCAGCGTCCAGGAAAGGGTCTGGAGTGG
 190 200 210 220 230 240

L S M I W G D G N T D Y N S A L K S R L
 CTGGGAATGATTTTGGGGTGTATGGAACACAGACTATAATTCAGCTCTCAAATCCAGACTG
 250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
 AGCATCAGCAAGGACAACTCCAAAGAGCCAGTTTTCTTAAAAATGAACAGTCTGCACACT
 310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
 GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTACTGGGGC
 370 380 390 400 410 420

Q G T T V T V S S
 CAAGGCACCCAGGTACCGTGTCTCTCATAATAAGAGCTATCCCGGCTAAGCTCGAATTC
 430 440 450 460 470 480

SmaI

FIG. 13

PSW2

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HindIII AAGCTT

GCATGCAAAATTCATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
10 20 30 40 50 60

M K Y L L P T A A
A G L L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTATTACTCGCTGCGCAACCGGATGGCCCCAGGTGCAGCTGCAGGAGTCA
70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
GGACCTGGCCTGGTGGCGCGCTCACAGCGCTGTCATCAGATGCACCGTCTCAGGGTTC
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAAAGCGCTATGCTGTAAGCTGGCTGGCGAGCTCCAGGAAAGGGTCTGGAGTGG
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTTGGGCTGATGGAACACAGACTATAATTCAGCTCTCAAATCCAGACTG
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACTCCAGAGCGCAAGTTTTCTTAAAAATGAACAGTCTGCACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCGGCTACTACTGTGCGAGAGAGAGATTATAGGCTTGACTACTGGGGC
370 380 390 400 410 420

Q G T T V T V S S
CAAGGACCGAGCTGACCGTCTCTCATTAATTAAGAGCTCGAATTCGCCAAGCTTGCAATGC
430 440 450 460 470 480

M K Y L L P T A A A G
AAATTCATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCGCTGGA
490 500 510 520 530 540

L L L L A A Q P A M A D I V L T Q S P A
TTGTTATTACTCGCTGCGCAACCGGATGGCCGACATCGTCTGACTCAGTCTCCAGCC
550 560 570 580 590 600

S L S A S V G E T V T I T C R A S G N I
TCCCTTTCTGCGTCTGTGGGAGAACTGTCACCATCACATGTCGAGCAAGTGGGAATATT
610 620 630 640 650 660

H N Y L A W Y Q Q K Q G K S P Q L L V Y
CACAATTATTAGCATGGTATCAGCAGAAACAGGGAAATGCTCTCAGTCTCTGGTCTAT
670 680 690 700 710 720

FIG. 14a

00227-4922260

14/23

Y T T T L A D G V P S R F S G S G S G T
TATACAACAACCTTAGCAGATGGTGTGCCATCAAGGTTCAAGTGGCAGTGGATCAGGAACA
730 740 750 760 770 780

Q Y S L K I N S L Q P E D F G S Y Y C Q
CAATATTCTCTCAAGATCAACAGCCTGCAACCTGAAGATTTGGGAGTTATTACTGTCAA
790 800 810 820 830 840

H F W S T P R T F G G G T K L E I K R
CATTTTGGAGTACTCCTCGGACCTTCGGTGGAGGACCAAGCTGGAATCAAACGGTAA
850 860 870 880 890 900

TAAGAGCTCGAATTC
910

FIG. 14 b

PSWHPOLYMYC

HindIII site AAGCTT

M K Y L L P T A A
GCATGCAAAATTCTATTTCAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q
GCTGGATTGTTATTACTCGGCTGCCCAACCAGCGATGGCCCAGGTGCAGCTGCAG
70 80 90 100 110 PstI

Polylinker

TCTAGA GTCGAC CTCGAG
XbaI SalI XhoI

MYC PEPTIDE

V T V S S E O K L I S E E D L N * *
GGTCACCGTCTCCTCAGAACAAAACTCATCTCAGAAGAGGATCTGAATTAATAA
BstEII

GGGCTAACCTCGAATTC

FIG. 15

09722364-112800

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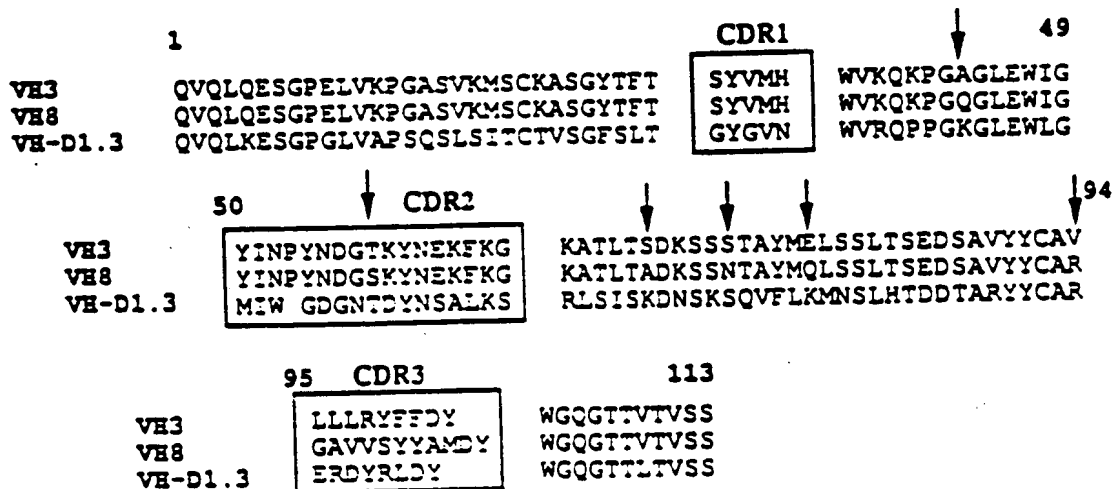


FIG. 16

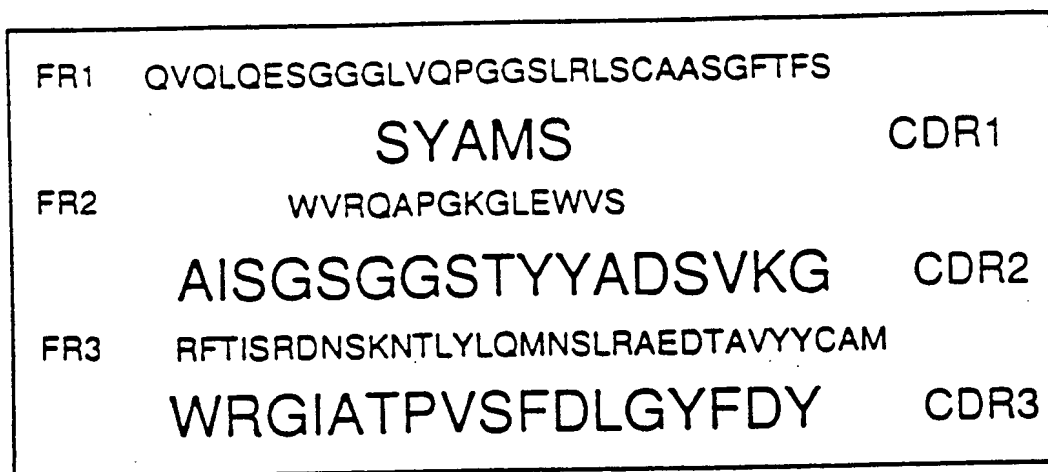


FIG. 17

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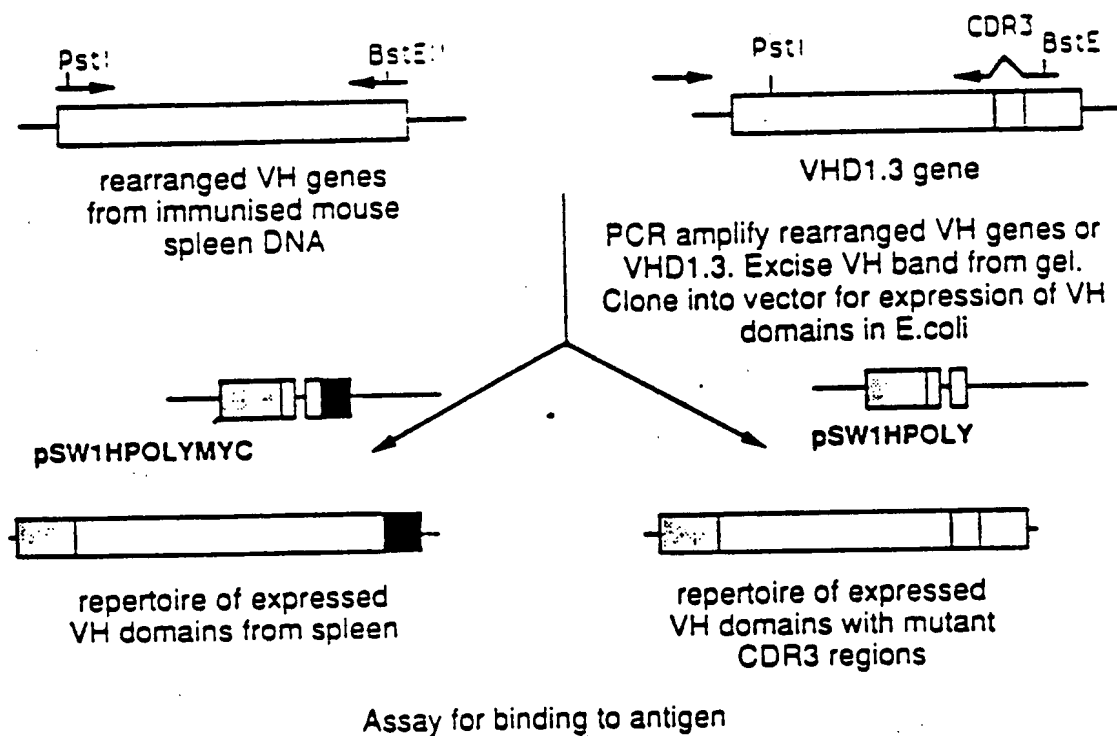


FIG. 18

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M K Y L L P T
AAGCTTGCATGCAAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACG
10 20 30 40 50 60
A A A G L L L L A A Q P A M A Q V Q L Q
GCAGCCGCTGGATTGTTATTACTGCTGCCCAACCAGCGATGGCCGAGGTGCAGCTGCAG
70 80 90 100 110 120
E S G P G L V A P S Q S L S I T C T V S
GAGTCAGGACCTGGCCTGGTGGCCGCTCACAGAGCCTGTCCATCACATGCCACGCTCTCA
130 140 150 160 170 180
G F S L T G Y G V N W V R Q P P G K G L
GGTTTCTCATTAACCGGCTATGGTGTAAGTGGGTTGCCAGCCTCCAGGAAGGGTCTG
190 200 210 220 230 240
E W L G M I W G D G N T D Y N S A L K S
GAGTGGCTGGGAATGATTGGGGTGATGGAAACACAGACTATAATTCAGCTCTCAAATCC
250 260 270 280 290 300
R L S I S K D N S K S Q V F L K M N S L
AGACTGAGCATCAGCAAGGACAACTGCAAGAGCCCAAGTTTCTTAAAAATGAACAGTCTG
310 320 330 340 350 360
H T D D T A R Y Y C A R E R D Y R L D Y
CACACTGATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTAC
370 380 390 400 410 420
W G Q G T T V T V S S G G G A P A A A P
TGGGGCAAGGCCACCGGCTCAGGCTCTGCTCAGGTGGTGGTGGTCCAGCAGCTGCACCT
430 440 450 460 470 480
A G G G C V Q L K E S G P G L V A P S Q
GCTGGAGGAGGACAGGTGCAGCTGAAGGAGTCAGGACCTGGCCCTGGTGGCCGCTCACAG
490 500 510 520 530 540
S L S I T C T V S G F S L T G Y G V N W
AGCCTGTCCATCACATGCCAGCTCTCAGGGTTCTCATTAACCGGCTATGGTGTAAGTGG
550 560 570 580 590 600
V R Q P P G K G L E W L G M I W G D G N
GTTGCCAGCCTCCAGGAAGGGTCTGGAGTGGCTGGGAATGATTTGGGGTGATGGAAC
610 620 630 640 650 660
T D Y N S A L K S R L S I S K D N S K S
ACAGACTATAATTCAGCTCTCAAATCCAGACTGAGCATCAGCAAGGACAACTCCAAGAGC
670 680 690 700 710 720
Q V F L K M N S L H T D D T A R Y Y C A
CAAGTTTTCTTAAAAATGAACAGTCTGCACACTGATGACACAGCCAGGTACTACTGTGCC
730 740 750 760 770 780
R E R D Y R L D Y W G Q G T T V T V S S
AGAGAGAGAGATTATAGGCTTGACTACTGGGGCCAAGGCACCGGTACCGTCTCTCTCA
790 800 810 820 830 840
TAATAAGAGCTC
850

FIG. 20

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003277-4922760

[illegible]

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FIG. 21c

Questions
Answers
Exercises
Problems
References
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Q V Q L Q E S G P G L V Q P S Q S L S I
 CAGGTGCAGCTGCAGGAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATC
 10 20 30 40 50 60

T C T V S G F S L T S Y G V H W V R Q S
 ACCTGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGTGTACACTGGGTTCCGCCAGTCT
 70 80 90 100 110 120

P G K G L E W L G M I W G D G N T D Y N
 CCAGGAAAGGGTCTGGAGTGGCTGGGAATGATTGGGGTGATGGAAACACAGACTATAAT
 130 140 150 160 170 180

S A L K S R L S I S K D N S K S Q V F L
 TCAGCTCTCAAATCCAGACTGAGCATCAGCAAGGACAACCTCCAAGAGCCAAGTTTCTTA
 190 200 210 220 230 240

K M N S L H T D D T A R Y Y C A R E R D
 AAAATGAACAGTCTTSCACACTGATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGAT
 250 260 270 280 290 300

Y R L D Y W G Q G T T V T V S S
 TATAGGCTTGACTACTGGGGCCAGGGGACCACGGTCACCGTCTCTCTCA
 310 320 330 340

FIG. 23